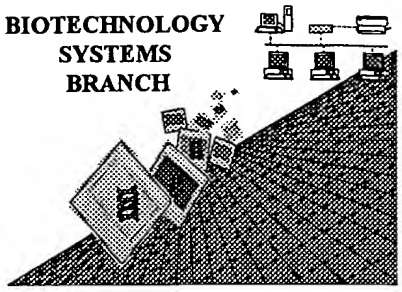
Exhibit B

Draper

FILE COPY

RAW SEQUENCE LISTING ERROR REPORT



FILE COPY

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 08/484,312

Art Unit / Team No. : 1644

Date Processed by STIC: 3/22/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/484,312*

DATE: 03/22/1999
TIME: 13:46:59

INPUT SET: S31121.raw

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

Does Not Comply
Corrected Diskette Needed

```
     1                                SEQUENCE LISTING
     2
     3  (1)    General Information:
     4
     5  (i) APPLICANT: Hauptman, et al.
     6
     7  (ii) TITLE OF INVENTION: TNF RECEPTORS, TNF BINDINGBINDING PROTEINS, AND DNAs CODIN
     8
-->  9  (iii) NUMBER OF SEQUENCES:64
    10
    11  (iv) CORRESPONDENCE ADDRESS:
    12  (A)ADDRESSEE:John J. McDonnell
    13  (B)STREET:300 S. Wacker Drive
    14  (C)CITY:Chicago
    15  (D)STATE:IL
    16  (E)COUNTRY:USA
    17  (F)ZIP:60606
    18
    19  (v) COMPUTER READABLE FORM:
    20  (A) MEDIUM TYPE: Floppy disk
    21  (B) COMPUTER: IBM PC compatible
    22  (C) OPERATING SYSTEM: PC-DOS/MS-DOS
    23  (D) SOFTWARE:ASCII
    24
    25  (vi) CURRENT APPLICATION DATA:
    26  (A) APPLICATION NUMBER:08/484,312
    27  (B) FILING DATE:June 7, 1995
    28  (C) CLASSIFICATION:
    29
    30  (viii) ATTORNEY/AGENT INFORMATION:
    31  (A) NAME:John J. McDonnell
    32  (B) REGISTRATION NUMBER:  26,949
    33  (C) REFERENCE/DOCKET NUMBER:98,385-A
    34
    35  (ix) TELECOMMUNICATION INFORMATION:
    36  (A) TELEPHONE:312-913-0001
    37  (B) TELEFAX:312-913-9808
    38
```

? ?

(0) 72 (p. 19)

see item 3 on Error Summary Sheet

Suggestion: Consult Sequence Rules for valid format

ERRORED SEQUENCES FOLLOW:

```
    39  (2) INFORMATION FOR SEQ ID NO:1:
```

present a hard return after each cumulative base total – all text must be visible

```
40
41  (i) SEQUENCE CHARACTERISTICS:
42  (A) LENGTH:1365 bases
43  (B) TYPE:nucleic acid
44  (C) STRANDEDNESS:single
45  (D) TOPOLOGY:linear
46
47  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
48
49  ATGGGCCTCT CCACCGTGCC TGACCTGCTG CTGCCACTGG TGCTCCTGGA   50  GCTGTTGGTG GGAATATACC
50
```

```
51  (2) INFORMATION FOR SEQ ID NO:2:
52
53  (i) SEQUENCE CHARACTERISTICS:
54  (A) LENGTH:483 bases
55  (B) TYPE:nucleic acid
56  (C) STRANDEDNESS:single
57  (D) TOPOLOGY:linear
58
59  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
60
61  GATAGTGTGT GTCCCCAAGG AAAATATATC CACCCTCAAA ATAATTCGAT   50 TTGCTGTACC AAGTGCCACA A
62
```

base error

```
63  (2) INFORMATION FOR SEQ ID NO:3:
64
65  (i) SEQUENCE CHARACTERISTICS:
66  (A) LENGTH:455 amino acids
67  (B) TYPE:polypeptide
68  (D) TOPOLOGY: Insert MANDATORY Feeding response for all sequence types
69  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
70
71  Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu
72                   5                  10                  15
73  Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu
74                  20                  25                  30
75  Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro
76                  35                  40                  45
77  Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr
78                  50                  55                  60
79  Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro
80                  65                  70                  75
81  Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr
82                  80                  85                  90
83  Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys
84                  95                 100                 105
85  Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
86                 110                 115                 120
87  Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr
88                 125                 130                 135
89  Trap Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu
90                 140                 145                 150
```

invalid – the only valid response for an amino acid sequence is "amino acid"

These are global errors

```
 91  Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val
 92                  155                 160                 165
 93  Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val
 94                  170                 175                 180
 95  Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys
 96                  185                 190                 195
 97  Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr
 98                  200                 205                 210
 99  Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu Leu
100                  215                 220                 225
101  Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
102                  230                 235                 240
103  Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys
104                  245                 250                 255
105  Glu Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn
106                  260                 265                 270
107  Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe
108                  275                 280                 285
109  Ser Pro Val Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr
110                  290                 295                 300
111  Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala
112                  305                 310                 315
113  Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala
114                  320                 325                 330
115  Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp Ser Ala
116                  335                 340                 345
117  His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu Tyr
118                  350                 355                 360
119  Ala Val Val Glu Asn Val Pro Pro Leu Arg Trp Lys Glu Phe Val
120                  365                 370                 375
121  Arg Arg Leu Gly Leu Ser Asp His Glu Ile Asp Arg Leu Glu Leu
122                  380                 385                 390
123  Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln Tyr Ser Met Leu Ala
124                  395                 400                 405
125  Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala Thr Leu Glu Leu
126                  410                 415                 420
127  Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly Cys Leu Glu
128                  425                 430                 435
129  Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro Pro Ala
130                  440                 445                 450
131  Pro Ser Leu Leu Arg
132                  455
133
```

```
134  (2) INFORMATION FOR SEQ ID NO:4:
135
136  (i) SEQUENCE CHARACTERISTICS:
137  (A) LENGTH:161 amino acids
138  (B) TYPE:polypeptide
139
140  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
141
142  Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn
```

Same error

```
143                    5                  10                  15
144  Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn
145                   20                  25                  30
146  Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu
147                   35                  40                  45
148  Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu
149                   50                  55                  60
150  Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser
151                   65                  70                  75
152  Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn
153                   80                  85                  90
154  Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn
155                   95                 100                 105
156  Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
157                  110                 115                 120
158  Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg
159                  125                 130                 135
160  Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu
161                  140                 145                 150
162  Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu Asn
163                  155                 160
164
```

```
165  (2) INFORMATION FOR SEQ ID NO:5:
166
167  (i) SEQUENCE CHARACTERISTICS:
168  (A) LENGTH:157 bases
169  (B) TYPE:nucleic acid
170  (C) STRANDEDNESS:single
171  (D) TOPOLOGY:linear
172
173  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
174
175  CAGGGGAAA ATATTCACCC TCAAATAAT TCGATTTGCT GTACCAAGTG     50 CCACAAAGG AAACTACTTG TA
176
```

insert hard returns

```
177  (2) INFORMATION FOR SEQ ID NO:6:
178
179  (i) SEQUENCE CHARACTERISTICS:
180  (A) LENGTH:13 amino acids
181  (B) TYPE:polypeptide
182
183  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
184
185  Asp Ser Val Xaa Pro Gln Gly Lys Tyr Ile His Pro Gln
186                   5                  10
187
```

add (D) TOPOLOGY: and sequence

```
188  (2) INFORMATION FOR SEQ ID NO:7:
189
190  (i) SEQUENCE CHARACTERISTICS:
191  (A) LENGTH:11 amino acids
192  (B) TYPE:polypeptide
```

same error

193
--> **194** **(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:**
195
196 Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys
197 5 10
198

---

199 (2) INFORMATION FOR SEQ ID NO:8:
200
201 (i) SEQUENCE CHARACTERISTICS:
--> **202** **(A) LENGTH:12 amino acids**
--> **203** **(B) TYPE:polypeptide**
204
--> **205** **(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:**
206
207 Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys
208 5 10
209

same error

---

210 (2) INFORMATION FOR SEQ ID NO:9:
211
212 (i) SEQUENCE CHARACTERISTICS:
--> **213** **(A) LENGTH:13 amino acids**
--> **214** **(B) TYPE:polypeptide**
215
--> **216** **(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:**
217
218 Tyr Ile His Pro Gln Xaa Asn Ser Ile Xaa Xaa Xaa Lys
219 5 10
220
221 (11) INFORMATION FOR SEQ ID NO:10:
222
223 (i) SEQUENCE CHARACTERISTICS:
--> **224** **(A) LENGTH:14 amino acids**
--> **225** **(B) TYPE:polypeptide**
226
--> **227** **(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:**
228
229 Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn Asn Lys
230 5 10
231

same

(2) ← use these numbers for all sequences

--> **232** **(2) INFORMATION FOR SEQ ID NO:11:**
233
234 (i) SEQUENCE CHARACTERISTICS:
--> **235** **(A) LENGTH:15 amino acids**
--> **236** **(B) TYPE:polypeptide**
237
--> **238** **(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:**
239
240 Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg
241 5 10 15
242

same

```
      292
      293   (i) SEQUENCE CHARACTERISTICS:
-->   294   (A) LENGTH:18 amino acids
-->   295   (B) TYPE:polypeptide
      296
-->   297   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
      298
      299   Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr
      300                    5                  10                  15
      301   Xaa Xaa Arg
      302
      303
```

none

```
      304   (2) INFORMATION FOR SEQ ID NO:17:
      305
      306   (i) SEQUENCE CHARACTERISTICS:
-->   307   (A) LENGTH:14 amino acids
-->   308   (B) TYPE:polypeptide
      309
-->   310   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
      311
      312   Gln Asn Thr Val Cys Thr Xaa His Ala Gly Phe Phe Leu Arg
      313                    5                  10
      314
```

none

```
      315   (2) INFORMATION FOR SEQ ID NO:18:
      316
      317   (i) SEQUENCE CHARACTERISTICS:
-->   318   (A) LENGTH:14 amino acids
-->   319   (B) TYPE:polypeptide
      320
-->   321   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
      322
      323   Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu Asn
      324                    5                  10
      325
```

none

```
      326   (2) INFORMATION FOR SEQ ID NO:19:
      327
      328   (i) SEQUENCE CHARACTERISTICS:
-->   329   (A) LENGTH:13 amino acids
-->   330   (B) TYPE:polypeptide
      331
-->   332   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
      333
      334   Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln
      335                    5                  10
      336
```

none

```
      481   (2) INFORMATION FOR SEQ ID NO:32:
      482
      483   (i) SEQUENCE CHARACTERISTICS:
-->   484   (A) LENGTH:14 amino acids
```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH:13 amino acids
(B) TYPE:polypeptide

same

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gly Thr Tyr Ley Tyr Asn Asp Cys Pro Gly Pro Gly Gln
5 10

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH:13 amino acids
(B) TYPE:polypeptide

same

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Glu Met Gly Gln Val Glu Ile Ser Xaa Xaa Xaa Val Asp
5 10

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH:20 amino acids
(B) TYPE:polypeptide

same

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg
5 10 15
Asp Thr Val Cys Gly
20

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH:19 amino acids
(B) TYPE:polypeptide

same

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Tyr Ile His Pro Gln Xaa Asn Ser Ile Cys Cys Thr Lys Cys His
5 10 15
Lys Gly Xaa Tyr

(2) INFORMATION FOR SEQ ID NO:16:

same

--> **485** **(B) TYPE:polypeptide**
486
--> **487** **(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:**
488
489 Glu Cys Gly Ser Gly Ser Phe Thr Ala Ser Glu Asn Asn Lys
490 5 10
491

---

492 (2) INFORMATION FOR SEQ ID NO:33:
493
494 (i) SEQUENCE CHARACTERISTICS:
--> **495** **(A) LENGTH:14 amino acids**
--> **496** **(B) TYPE:polypeptide**
497
--> **498** **(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:**
499
500 Glu Cys Gly Ser Gly Ser Phe Thr Ala Ser Cys Asn Asn Lys
501 5 10
502

same

---

647 (2) INFORMATION FOR SEQ ID NO:46:
648
649 (i) SEQUENCE CHARACTERISTICS:
--> **650** **(A) LENGTH:51 amino acids**
--> **651** **(B) TYPE:polypeptide**
652
--> **653** **(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:**
654
655 Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr
656 5 10 15
657 Lys Cys His Lys Gly Thr Tyr Ley Tyr Asn Asp Cys Pro Gly Pro
658 20 25 30
659 Gly Gln Asp Thr Asp Cys Arg Gly Cys Glu Ser Gly Ser Phe Thr
660 35 40 45
661 Ala Ser Glu Asn Asn Lys
662 50
663

same

---

664 (2) INFORMATION FOR SEQ ID NO:47:
665
666 (i) SEQUENCE CHARACTERISTICS:
--> **667** **(A) LENGTH:158 bases**
668 (B) TYPE:nucleic acid
669 (C) STRANDEDNESS:single
670 (D) TOPOLOGY:linear
671
672 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:
673
674 CAGGGGAAAT ATATTCACCC TCAAAATAAT TCGATTTCGT GTACCAAGTC 50 GCACAAAGGA ACCTACTTGT A
675

---

762 (2) INFORMATION FOR SEQ ID NO:55:
763

764 (i) SEQUENCE CHARACTERISTICS:
--> 765 **(A) LENGTH:63 bases**
766 (B) TYPE:nucleic acid
767 (C) STRANDEDNESS:single
768 (D) TOPOLOGY:linear
769
770 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:
771
772 AGCTCTAGAG ATTCGCGGCC GCTCGAGGTA CCGGATCCAT CGATGTCGAC 50 CTGCAGAAGC TTG
773

---

774 (2) INFORMATION FOR SEQ ID NO:56:
775
776 (i) SEQUENCE CHARACTERISTICS:
--> 777 **(A) LENGTH:64 bases**
778 (B) TYPE:nucleic acid
779 (C) STRANDEDNESS:single
780 (D) TOPOLOGY:linear
781
782 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:
783
784 CTAGCAAGCT TCTGCAGGTC GACATCGATG GATCCGGTAC CTCGAGCGGC 50 CGCGAATTCT CTAG
785

---

810 (2) INFORMATION FOR SEQ ID NO:59:
811
812 (i) SEQUENCE CHARACTERISTICS:
--> 813 **(A) LENGTH:81 bases**
814 (B) TYPE:nucleic acid
815 (C) STRANDEDNESS:single
816 (D) TOPOLOGY:linear
817
818 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:
819
820 CACAGTCGAC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT 50 CAAACAGACA CCATGGGCCT C
821

---

870 (2) INFORMATION FOR SEQ ID NO:64:
871
872 (i) SEQUENCE CHARACTERISTICS:
--> 873 **(A) LENGTH:30 bases** 18 shown
874 (B) TYPE:nucleic acid
875 (C) STRANDEDNESS:single
876 (D) TOPOLOGY:linear
877
878 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:
879
880 GTCCAATTAT GTCACACC 18
881

---

882 (2) INFORMATION FOR SEQ ID NO:65:
883
884 (i) SEQUENCE CHARACTERISTICS:

--> 885 **(A) LENGTH:1334 bases**
886 (B) TYPE:nucleic acid
887 (C) STRANDEDNESS:single
888 (D) TOPOLOGY:linear
889
890 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:
891
892 GAATTCTCTG GACTGAGGCT CCAGTTCTGG CCTTTGGGGT TCAAGATCAC 50 TGGGACCAGG CCGTGAT
893
--> 894 **TAGCTGTCTG GC** 212
895
896 ATG GGC CTC TCC ACC GTG CCT GAC CTG CTG CTG CCA CTG GTG TTC 257
897 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu
898 5 10 15
899
900 CTG GAG CTG TTG GTG GGA ATA TAC CCC TCA GGG GTT ATT GGA CTG 302
901 Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu
902 20 25 30
903
904 GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA GAT AGT GTG TGT CCC 347
905 Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro
906 35 40 45
907
908 CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG ATT TGC TGT ACC 392
909 Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr
910 50 55 60
911
912 AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT CCA GGC CCG 437
913 Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro
914 65 70 75
915
916 GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC TCC TTC ACC 482
917 Gly Gln Asp The Asp Cys Arg Glu Cys Gly Ser Gly Ser Phe Thr
918 80 85 90
919
920 GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC AAA TGC 527
921 Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys
922 95 100 105
923
924 CGA AAG GAA ATC GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC 572
925 Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
926 110 115 120
927
928 CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT 617
929 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr
930 125 130 135
931
932 TGG AGT GAA AAC CTTTTC CAG TGC TTC AAT TGC AGC CTC TGC CTC 662
933 Trp Ser Glu Asn LeuPhe Gln Cys Phe Asn Cys Ser Leu Cys Leu
934 140 145 150
935
936 AAT GGG ACC GTG CAC CTC TCC TGC CAG GAG AAA CAG AAC ACC GTG 707
937 Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val

spaces appear in submitted file - if there is a gap in the sequence, separate sequences must be shown (see 1.822(b) of Sequence Rules)

```
938                 155                 160                 165
939
940  TGC ACC TGC CAT GCA GGT TTC TTT CTA AGA GAA AAC GAG TGT GTC  752
941  Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val
942                 170                 175                 180
943
944  TCC TGT AGT AAC TGT AAG AAA AGC CTG GAG TGC AGG AAG TTG TGC  797
945  Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys
946                 185                 190                 195
947
948  CTA CCC CAG ATT GAG AAT GTT AAG GGC ACT GAG GAC TCA GGC ACC  842
949  Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr
950                 200                 205                 210
951
952  ACA GTG CTG TTG CCC CTG GTC ATT TTC TTT GGT CTT TGC CTT TTA  887
953  Thr Val Leu Leu ProLeu Val Ile Phe Phe Gly Leu Cys Leu Leu
954                 215 ) gap ?         220                 225
955
956  TCC CTC CTC TTC ATT GGT TTA ATG TAT CGC TAC CAA CGG TGG AAG  932
957  Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
958                 230                 235                 240
959
960  TCC AAG CTC TAC TCC ATT GTT TGT GGG AAA TCG ACA CCT GAA AAA  977
961  Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys
962                 245                 250                 255
963
964  GAG GGG GAG CTT GAA GGA ACT ACT ACT AAG CCC CTG GCC CCA AAC 1022
965  Glu Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn
966                 260                 265                 270
967
968  CCA AGC TTC AGT CCC ACT CCA GGC TTC ACC CCC ACC CTG GGC TTC 1067
969  Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe
970                 275                 280                 285
971
972  AGT CCC GTG CCC AGT TCC ACC TTC ACC TCC AGC TCC ACC TAT ACC 1112
973  Ser Pro Val Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr
974                 290                 295                 300
975
976  CCC GGT GAC TGT CCC AAC TTT GCG GCT CCC CGC AGA GAG GTG GCA 1157
977  Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala
978                 305                 310                 315
979
980  CCA CCC TAT CAG GGG GCT GAC CCC ATC CTT GCG ACA GCC CTC GCC 1202
981  Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala
982                 320                 325                 330
983
984  TCC GAC CCC ATC CCC AAC CCC CTT CAG AAG TGG GAG GAC AGC GCC 1247
985  Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp Ser Ala
986                 335                 340                 345
987
988  CAC AAG CCA CAG AGC CTA GAC ACT GAT GAC CCC GCG ACG CTG TAC 1292
989  His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu Tyr
990                 350                 355                 360
```

```
      991
      992  GCC GTG GTG GAG AAC GTG CCC CCG TTG CGC TGG AAGGAATTC       1334
      993  Ala Val Val Glu Asn Val Pro Pro Leu Arg Trp
      994                  365                 370
      995
      996
```

```
      997  (2) INFORMATION FOR SEQ ID NO:66:
      998
      999  (i) SEQUENCE CHARACTERISTICS:
-->  1000  (A) LENGTH:371 amino acids
-->  1001  (B) TYPE:polypeptide
     1002
-->  1003  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:
     1004
     1005  Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu
     1006                   5                  10                  15
     1007  Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu
     1008                  20                  25                  30
     1009  Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro
     1010                  35                  40                  45
     1011  Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr
     1012                  50                  55                  60
     1013  Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro
     1014                  65                  70                  75
     1015  Gly Gln Asp The Asp Cys Arg Glu Cys Gly Ser Gly Ser Phe Thr
     1016                  80                  85                  90
     1017  Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys
     1018                  95                 100                 105
     1019  Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
     1020                 110                 115                 120
     1021  Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr
     1022                 125                 130                 135
     1023  Trp Ser Glu Asn LeuPhe Gln Cys Phe Asn Cys Ser Leu Cys Leu
     1024                 140 Lgor?           145                 150
     1025  Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val
     1026                 155                 160                 165
     1027  Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val
     1028                 170                 175                 180
     1029  Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys
     1030                 185                 190                 195
     1031  Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr
     1032                 200                 205                 210
     1033  Thr Val Leu Leu ProLeu Val Ile Phe Phe Gly Leu Cys Leu Leu
     1034                 215 L gor?          220                 225
     1035  Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
     1036                 230                 235                 240
     1037  Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys
     1038                 245                 250                 255
     1039  Glu Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn
     1040                 260                 265                 270
     1041  Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe
     1042                 275                 280                 285
```

```
1043  Ser Pro Val Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr
1044                  290                 295                 300
1045  Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala
1046                  305                 310                 315
1047  Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala
1048                  320                 325                 330
1049  Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp Ser Ala
1050                  335                 340                 345
1051  His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu Tyr
1052                  350                 355                 360
1053  Ala Val Val Glu Asn Val Pro Pro Leu Arg Trp
1054                  365                 370
1055
```

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1056  (2) INFORMATION FOR SEQ ID NO:67:
1057
1058  (i) SEQUENCE CHARACTERISTICS:
--> 1059  (A) LENGTH:6464 bases
1060  (B) TYPE:nucleic acid
1061  (C) STRANDEDNESS:single
1062  (D) TOPOLOGY:linear
1063
1064  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:
1065
1066  TCGACATTGA TTATTGACTA GTTATTAATA GTAATCAATT ACGGGGTCAT    50
1067  TAGTTCATAG CCCATATATG GAGTTCCGCG TTACATAACT TACGGTAAAT   100 GGCCCGCCTC GCTGACCGCC C
1068  CTGGCATTAT GCCCAGTACA TGACCTTATG GGACTTTCCT ACTIGGCAGT   350 ACATCTACGT ATTAGTCATC G
1069  AGAACCCACT GCTTAACTGG CTTATCGAAA TTAATACGAC TCACTATAGG   650 GAGACCCAAG CTTCTGCAGG T
1070  AGGTTTTACT TGCTTTAAAA AACCTCCCAC ACCTCCCCCT GAACCTGAAA 1250 CATAAAATGA ATGCAATTGT T
1071  GTTAAAAGAT GTATCCTGGA CCTGCCAGAC CTGGCCATTC ACGTAAACAG 1550 AAGATTCCGC CTCAAGTTCC G
1072  CCCACCACCT GGCCCCGCCC CGTTGAGGAC AGAAGAAACC CCGGGCAGCC 1850 GCAGCCAAGG CGGACGGGTA G
1073  GCGGCCACGC CGGACTGGGC GGGGCCGGCC TGGTGGAGGC GGAGTCTGAC 2150 CTCGTGGAGG CGGGGCCTCT G
1074  TGGCTGGATT GGGTTAGGGA AACCGAGGCG GTTCGCTGAA TCGGGTCGAG 2450 CACTTGGCGG AGACGCGCGG G
1075  GAACGAGTTC AAGTACTTCC AAAGAATGAC CACCACCTCC TCAGTGGAAG 2750 GTAAACAGAA CCTGGTGATT A
1076  AGGCCATCTC AGACTCTTTG TGACAAGGAT CATGCAGGAA TTTGAAAGTG 3050 ACACGTTCTT CCCAGAAATT G
1077  GCAGAGCTAG AACTCAGACT TTAAAGAAAA TTAGATCAAA GTAGAGACTG 3650 AATTATTCTG CACATCAGAC T
1078  ATGCATCTCA ATTAGTCAGC AACCAGGTGT GGAAAGTCCC CAGGCTCCCC 4000 AGCAGGCAGA AGTATGCAAA G
1079  CTGTAGCGGC GCATTAAGCG CGGCGGGTGT GGTGGTTACG CGCAGCGTGA 4255 CCGCTACACT TGCCAGCGCC C
1080  GTCGCCCTTA TTCCCTTTTT TGCGGCATTT TGCCTTCCTG TTTTTGCTCA 4850 CCCAGAAACG CTGGTGAAAG T
1081  GAAAAGCATC TTACGGATGG CATGACAGTA AGAGKATTAT GCAGTGCTGC 5150 CATAACCATG AGTGATAACA C
1082  TGGATGGAGG CGGATAAAGT TGCAGGACCA CTTCTGCGCT CGGCCCTTCC 5450 GGCTGGCTGG TTTATTGCTG A
1083  AAAAGGATCT AGGTGAAGAT CCTTTTTGAT AATCTCATGA CCAAAATCCC 5750 TTAACGTGAG TTTTCGTTCC A
1084  GTAGCACCGC CTACATACCT CGCTCTGCTA ATCCTGTTAC CAGTGGCTGC 6100 TGCCAGTGGC GATAAGTCGT G
1085  GGAAACGCCT GGTATCTTTA TAGTCCTGTC GGGTTTCGCC ACCTCTGACT 6400 TGAGCGTCGA TTTTTGTGAT G
1086
```

```
1087  (2) INFORMATION FOR SEQ ID NO:68:
1088
1089  (i) SEQUENCE CHARACTERISTICS:
--> 1090  (A) LENGTH:2173 bases
1091  (B) TYPE:nucleic acid
1092  (C) STRANDEDNESS:single
1093  (D) TOPOLOGY:linear
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GAATTCCTTT TCTCCGAGTT TTCTGAACTC TGGCTCATGA TCGGGCTTAC 50 TGGATACGAG AATCCTG

--> **ATG GGT CTC CCC ATC GTG CCT GGC CTG CTG CTG TCA CTG GTG CTC 289**
Met Gly Leu Pro Ile Val Pro Gly Leu Leu Leu Ser Leu Val Leu
5 10 15

CTG GCT CTG CTG ATG GGG ATA CAC CCA TCA GGG GTC ACC GGA CTG 334
Leu Ala Leu Leu Met Gly Ile His Pro Ser Gly Val Thr Gly Leu
20 25 30

GTT CCT TCT CTT GGT GAC CGG GAG AAG AGG GAT AAT TTG TGT CCC 379
Val Pro Ser Leu Gly Asp Ara Glu Lys Arg Asp Asn Leu Cys Pro
35 40 45

CAG GGA AAG TAT GCC CAT CCA AAG AAT AAT TCC ATC TGC TGC ACC 424
Gln Gly Lys Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cvs Thr
50 55 60

AAG TGC CAC AAA GGA ACC TAC TTG GTG AGT GAC TGT CCA AGC CCA 469
Lys Cys His Lys Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro
65 70 75

GGG CAG GAA ACA GTC TGC GAG CTC TCT CAT AAA GGC ACC TTT ACA 514
Gly Gln Glu Thr Val Cys Glu Leu Ser His Lys Gly Thr Phe Thr
80 85 90

GCT TCG CAG AAC CAC GTC AGA CAG TGT CTC AGT TGC AAG ACA TGT 559
Ala Ser Gln Asn His Val Arg Gln Cys Leu Ser Cys Lys Thr Cys
95 100 105

CGG AAA GAA ATG TTC CAG GTG GAG ATT TCT CCT TGC AAA GCT GAC 604
Arg Lys Glu Yet Phe Gln Val Glu Ile Ser Pro Cys Lys Ala Asp
110 115 120

--> **ATG GAC ACC GTG TGT GGC TGC AAG AAG AAC CAA TTC CAG CGC TAC 649**
Met Asp Thr Val Cys Gly Cys Lys Lys Asn Gln Phe Gln Arg Tyr
125 130 135

CTG AGT GAG ACG CAT TTC CAG TGT GTG GAC TGC AGC CCC TGC TTC 694
Leu Ser Glu Thr His Phe Gln Cys Val Asp Cys Ser Pro Cys Phe
140 145 150

AAT GGC ACC GTG ACA ATC CCC TGT AAG GAG AAA CAG AAC ACC GTG 739
Asn Gly Thr Val Thr Ile Pro Cys Lys Glu Lys Gln Asn Thr Val
155 160 165

TGT AAC TGC CAC GCA GGA TTC TTT CTA AGC GGA AAT GAG TGC ACC 784
Cys Asn Cys His Ala Gly Phe Phe Leu Ser Gly Asn Glu Cys Thr
170 175 180

```
1147  CCT TGC AGC CAC TGC AAG AAA AAT CAG GAA TGT ATG AAG CTG TGC  829
1148  Pro Cys Ser His Cys Lys Lys Asn Gln Glu Cys Met Lys Leu Cys
1149                  185                 190                 195
1150
1151  CTA CCT CCA GTT GCA AAT GTC ACA AAC CCC CAG GAC TCA GGT ACT  874
1152  Leu Pro Pro Val Ala Asn Val Thr Asn Pro Gln Asp Ser Gly Thr
1153                  200                 205                 210
1154
--> 1155  GCC GTC CTG TTG CCT CTG GTT ATC TTC CTA GGT CTT TGC CTT TTA  919
1156  Ala Val Leu Leu Pro Leu Val Ile Phe Leu Gly Leu Cys Leu Leu
1157                  215                 220                 225
1158
1159  TTC TTT ATC TGC ATC AGT CTA CTG TGC CGA TAT CCC CAG TGG AGG  964
1160  Phe Phe Ile Cys Ile Ser Leu Leu Cys Arg Tyr Pro Gln Trp Arg
1161                  230                 235                 240
1162
1163  CCC AGG GTC TAC TCC ATC ATT TGT AGG GAT TCA GCT CCT GTC AAA 1009
1164  Pro Arg Val Tyr Ser Ile Ile Cys Arg Asp Ser Ala Pro Val Lys
1165                  245                 250                 255
1166
1167  GAG GTG GAG GGT GAA GGA ATT GTT ACT AAG CCC CTA ACT CCA GCC 1054
1168  Glu Val Glu Gly Glu Gly Ile Val Thr Lys Pro Leu Thr Pro Ala
1169                  260                 265                 270
1170
1171  TCT ATC CCA GCC TTC AGC CCC AAC CCC GGC TTC AAC CCC ACT CTG 1099
1172  Ser Ile Pro Ala Phe Ser Pro Asn Pro Gly Phe Asn Pro Thr Leu
1173                  275                 280                 285
1174
1175  GGC TTC AGC ACC ACC CCA CGC TTC AGT CAT CCT GTC TCC AGT ACC 1144
1176  Gly Phe Ser Thr Thr Pro Arg Phe Ser His Pro Val Ser Ser Thr
1177                  290                 295                 300
1178
1179  CCC ATC AGC CCC GTC TTC GGT CCT AGT AAC TGG CAC AAC TTC GTG 1189
1180  Pro Ile Ser Pro Val Phe Gly Pro Ser Asn Trp His Asn Phe Val
1181                  305                 310                 315
1182
1183  CCA CCT GTA AGA GAG GTG GTC CCA ACC CAG GGT GCT GAC CCT CTC 1234
1184  Pro Pro Val Arg Glu Val Val Pro Thr Gln Gly Ala Asp Pro Leu
1185                  320                 325                 330
1186
1187  CTC TAC GGA TCC CTC AAC CCT GTG CCA ATC CCC GCC CCT GTT CGG 1279
1188  Leu Tyr Gly Ser Leu Asn Pro Val Pro Ile Pro Ala Pro Val Arg
1189                  335                 340                 345
1190
1191  AAA TGG GAA GAC GTC GTC GCG GCC CAG CCA CAA CGG CTT GAC ACT 1324
1192  Lys Trp Glu Asp Val Val Ala Ala Gln Pro Gln Arg Leu Asp Thr
1193                  350                 355                 360
1194
1195  GCA GAC CCT GCG ATG CTG TAT GCT GTG GTG GAT GGC GTG CCT CCG 1369
1196  Ala Asp Pro Ala Met Leu Tyr Ala Val Val Asp Gly Val Pro Pro
1197                  365                 370                 375
1198
1199  ACA CGC TGG AAG GAG TTC ATG CGG CTC CTG GGG CTG AGC GAG CAC 1414
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1200  Thr Arg Trp Lys Glu Phe Met Arg Leu Leu Gly Leu Ser Glu His
1201                  380                 385                 390
1202
1203  GAG ATC GAG CGG TTG GAG CTG CAG AAC GGG CGT TGC CTC CGC GAG 1459
1204  Glu Ile Glu Arc Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu
1205                  395                 400                 405
1206
1207  GCT CAT TAC AGC ATG CTG GAA GCC TGG CGG CGC CGC ACA CCG CGA 1504
1208  Ala His Tyr Ser Met Leu Glu Ala Trp Arg Arg Arg Thr Pro Arg
1209                  410                 415                 420
1210
1211  CAC GAG GCC ACG CTG GAC GTA GTG GGC CGC GTG CTT TGC GAC ATG 1549
1212  His Glu Ala Thr Leu Asp Val Val Gly Arg Val Leu Cys Asp Met
1213                  425                 430                 435
1214
1215  AAC CTG CGT GGC TGC CTG GAG AAC ATC CGC GAG ACT CTA GAA AGC 1594
1216  Asn Leu Arg Gly Cys Leu Glu Asn Ile Arg Glu Thr Leu Glu Ser
1217                  440                 445                 450
1218
1219  CCT GCC CAC TCG TCC ACG ACC CAC CTC CCG CGA TAAGGCCACA      1637
1220  Pro Ala His Ser Ser Thr Thr His Leu Pro Arg
1221                  455                 460
1222
1223  CCCCCACCTC AGGAACGGGA CTCGAAGGAC CATCCTGCTA GATGCCCTGC      1687 TTCCCTGTGA ACCTCCT
--> 1224  GGGAAGTGTG CCATCTGCTC CCAGACAGCT GAGGGTGCCA AAAGCCAGGA      1887
1225  GAGGTGATTG TGGAGAAAAA GCACAATCTA TCTGATACCC ACTTGGGATG      1937
1226  CAAGGACCCA AACAAAGCTT CTCAGGGCCT CCTCAGTTGA TTTCTGGGCC      1987
1227  CTTTTCACAG TAGATAAAAC AGTCTTTGTA TTGATTATAT CACACTAATG      2037
1228  GATGAACGGT TGAACTCCCT AAGGTAGGGG CAAGCACAGA ACAGTGGGGT      2087
1229  CTCCAGCTGG AGCCCCCGAC TCTTGTAAAT ACACTAAAAA TCTAAAAGTG      2137
1230  AAAAAAAAAA AAAAAAAAAA AAAAAAAAAG GAATTC                    2173
1231
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1232  (2) INFORMATION FOR SEQ ID NO:69:
1233
1234  (i) SEQUENCE CHARACTERISTICS:
--> 1235  (A) LENGTH:461 amino acids
--> 1236  (B) TYPE:polypeptide
1237
--> 1238  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:
1239
1240  Met Gly Leu Pro Ile Val Pro Gly Leu Leu Leu Ser Leu Val Leu
1241                    5                  10                  15
1242  Leu Ala Leu Leu Met Gly Ile His Pro Ser Gly Val Thr Gly Leu
1243                   20                  25                  30
1244  Val Pro Ser Leu Gly Asp Ara Glu Lys Arg Asp Asn Leu Cys Pro
1245                   35                  40                  45
1246
1247  Gln Gly Lys Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cvs Thr
1248                   50                  55                  60
1249  Lys Cys His Lys Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro
1250                   65                  70                  75
1251  Gly Gln Glu Thr Val Cys Glu Leu Ser His Lys Gly Thr Phe Thr
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1252                    80                  85                  90
1253  Ala Ser Gln Asn His Val Arg Gln Cys Leu Ser Cys Lys Thr Cys
1254                    95                  100                 105
1255  Arg Lys Glu Yet Phe Gln Val Glu Ile Ser Pro Cys Lys Ala Asp
1256                   110                 115                 120
1257  Met Asp Thr Val Cys Gly Cys Lys Lys Asn Gln Phe Gln Arg Tyr
1258                   125                 130                 135
1259  Leu Ser Glu Thr His Phe Gln Cys Val Asp Cys Ser Pro Cys Phe
1260                   140                 145                 150
1261  Asn Gly Thr Val Thr Ile Pro Cys Lys Glu Lys Gln Asn Thr Val
1262                   155                 160                 165
1263  Cys Asn Cys His Ala Gly Phe Phe Leu Ser Gly Asn Glu Cys Thr
1264                   170                 175                 180
1265  Pro Cys Ser His Cys Lys Lys Asn Gln Glu Cys Met Lys Leu Cys
1266                   185                 190                 195
1267  Leu Pro Pro Val Ala Asn Val Thr Asn Pro Gln Asp Ser Gly Thr
1268                   200                 205                 210
1269  Ala Val Leu Leu Pro Leu Val Ile Phe Leu Gly Leu Cys Leu Leu
1270                   215                 220                 225
1271  Phe Phe Ile Cys Ile Ser Leu Leu Cys Arg Tyr Pro Gln Trp Arg
1272                   230                 235                 240
1273  Pro Arg Val Tyr Ser Ile Ile Cys Arg Asp Ser Ala Pro Val Lys
1274                   245                 250                 255
1275  Glu Val Glu Gly Glu Gly Ile Val Thr Lys Pro Leu Thr Pro Ala
1276                   260                 265                 270
1277  Ser Ile Pro Ala Phe Ser Pro Asn Pro Gly Phe Asn Pro Thr Leu
1278                   275                 280                 285
1279  Gly Phe Ser Thr Thr Pro Arg Phe Ser His Pro Val Ser Ser Thr
1280                   290                 295                 300
1281  Pro Ile Ser Pro Val Phe Gly Pro Ser Asn Trp His Asn Phe Val
1282                   305                 310                 315
1283  Pro Pro Val Arg Glu Val Val Pro Thr Gln Gly Ala Asp Pro Leu
1284                   320                 325                 330
1285  Leu Tyr Gly Ser Leu Asn Pro Val Pro Ile Pro Ala Pro Val Arg
1286                   335                 340                 345
1287  Lys Trp Glu Asp Val Val Ala Ala Gln Pro Gln Arg Leu Asp Thr
1288                   350                 355                 360
1289  Ala Asp Pro Ala Met Leu Tyr Ala Val Val Asp Gly Val Pro Pro
1290                   365                 370                 375
1291  Thr Arg Trp Lys Glu Phe Met Arg Leu Leu Gly Leu Ser Glu His
1292                   380                 385                 390
1293  Glu Ile Glu Arc Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu
1294                   395                 400                 405
1295  Ala His Tyr Ser Met Leu Glu Ala Trp Arg Arg Arg Thr Pro Arg
1296                   410                 415                 420
1297  His Glu Ala Thr Leu Asp Val Val Gly Arg Val Leu Cys Asp Met
1298                   425                 430                 435
1299  Asn Leu Arg Gly Cys Leu Glu Asn Ile Arg Glu Thr Leu Glu Ser
1300                   440                 445                 450
1301  Pro Ala His Ser Ser Thr Thr His Leu Pro Arg
1302                   455                 460
1303
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1412  (2) INFORMATION FOR SEQ ID NO:71:
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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH:340 amino acids
(B) TYPE:polypeptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

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Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu
                  5                  10                  15
Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu
             20                  25                  30
Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro
         35                  40                  45

Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr
     50                  55                  60
Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro
 65                  70                  75
Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr
             80                  85                  90
Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys
         95                 100                 105
Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
    110                 115                 120
Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr
125                 130                 135
Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu
            140                 145                 150
Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val
        155                 160                 165
Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val
    170                 175                 180
Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys
185                 190                 195
Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr
            200                 205                 210
Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu Leu
        215                 220                 225
Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
    230                 235                 240
Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys
245                 250                 255
Glu Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn
            260                 265                 270
Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe
        275                 280                 285
Ser Pro Val Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr
    290                 295                 300
Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala
305                 310                 315
Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala
            320                 325                 330
Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys
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1466 335 340
1467
1468

1469 (2) INFORMATION FOR SEQ ID NO:72:
1470
1471 (i) SEQUENCE CHARACTERISTICS:
1472 (A) LENGTH:19 bases
1473 (B) TYPE:nucleic acid
1474 (C) STRANDEDNESS:single
1475 (D) TOPOLOGY:linear
1476
1477 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:
1478
1479 GTACTTGAAC TCGTTCCTG 19
1480
1481
1482
1483
1484
1485
1486
1487

last sequence in file

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/484,312*

DATE: 03/22/1999
TIME: 13:47:05

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9	Number of Sequences (64) Doesn't Equal Actual Count (71)	(iii) NUMBER OF SEQUENCES:64
42	Entered (1365) and Calc. Seq. Length (0) differ	(A) LENGTH:1365 bases
54	Entered (483) and Calc. Seq. Length (0) differ	(A) LENGTH:483 bases
66	Entered (455) and Calc. Seq. Length (0) differ	(A) LENGTH:455 amino acids
67	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
69	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
69	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
137	Entered (161) and Calc. Seq. Length (0) differ	(A) LENGTH:161 amino acids
138	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
140	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
140	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
168	Entered (157) and Calc. Seq. Length (0) differ	(A) LENGTH:157 bases
180	Entered (13) and Calc. Seq. Length (0) differ	(A) LENGTH:13 amino acids
181	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
183	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
183	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
191	Entered (11) and Calc. Seq. Length (0) differ	(A) LENGTH:11 amino acids
192	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
194	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
194	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
202	Entered (12) and Calc. Seq. Length (0) differ	(A) LENGTH:12 amino acids
203	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
205	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
205	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
213	Entered (13) and Calc. Seq. Length (0) differ	(A) LENGTH:13 amino acids
214	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
216	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
216	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
224	Entered (14) and Calc. Seq. Length (0) differ	(A) LENGTH:14 amino acids
225	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
227	Wrong Sequence Number	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
227	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
227	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
232	Sequence * missing	(12) INFORMATION FOR SEQ ID NO:11:
235	Entered (15) and Calc. Seq. Length (0) differ	(A) LENGTH:15 amino acids
236	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
238	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
238	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
246	Entered (13) and Calc. Seq. Length (0) differ	(A) LENGTH:13 amino acids
247	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
249	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
249	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
257	Entered (13) and Calc. Seq. Length (0) differ	(A) LENGTH:13 amino acids
258	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
260	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
260	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
268	Entered (20) and Calc. Seq. Length (0) differ	(A) LENGTH:20 amino acids
269	Wrong or Missing Sequence Type	(B) TYPE:polypeptide

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/484,312*

INPUT SET: S31121.raw

Line	Error	Original Text
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271	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
281	Entered (19) and Calc. Seq. Length (0) differ	(A) LENGTH:19 amino acids
282	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
284	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
284	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
294	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH:18 amino acids
295	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
297	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
297	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
307	Entered (14) and Calc. Seq. Length (0) differ	(A) LENGTH:14 amino acids
308	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
310	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
310	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
318	Entered (14) and Calc. Seq. Length (0) differ	(A) LENGTH:14 amino acids
319	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
321	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
321	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
329	Entered (13) and Calc. Seq. Length (0) differ	(A) LENGTH:13 amino acids
330	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
332	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
332	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
484	Entered (14) and Calc. Seq. Length (0) differ	(A) LENGTH:14 amino acids
485	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
487	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
487	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
495	Entered (14) and Calc. Seq. Length (0) differ	(A) LENGTH:14 amino acids
496	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
498	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
498	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
650	Entered (51) and Calc. Seq. Length (0) differ	(A) LENGTH:51 amino acids
651	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
653	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:
653	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:
667	Entered (158) and Calc. Seq. Length (0) differ	(A) LENGTH:158 bases
765	Entered (63) and Calc. Seq. Length (0) differ	(A) LENGTH:63 bases
777	Entered (64) and Calc. Seq. Length (0) differ	(A) LENGTH:64 bases
813	Entered (81) and Calc. Seq. Length (0) differ	(A) LENGTH:81 bases
873	Entered (30) and Calc. Seq. Length (18) differ	(A) LENGTH:30 bases
885	Entered (1334) and Calc. Seq. Length (1134) differ	(A) LENGTH:1334 bases
894	# of Sequences for line conflicts w/ running total	TAGCTGTCTG GC
1000	Entered (371) and Calc. Seq. Length (0) differ	(A) LENGTH:371 amino acids
1001	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
1003	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:
1003	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:
1059	Entered (6464) and Calc. Seq. Length (50) differ	(A) LENGTH:6464 bases
1090	Entered (2173) and Calc. Seq. Length (1727) differ	(A) LENGTH:2173 bases
1099	# of Sequences for line conflicts w/ running total	ATG GGT CTC CCC ATC GTG CCT GGC CTG CTG CT

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/484,312*

INPUT SET: S31121.raw

Line	Error	Original Text
1131	Wrong Nucleic Acid Designator	ATG GAC ACC GTG TGT GGC TGC AAG PAG AkC CA
1131	# of Sequences for line conflicts w/ running total	ATG GAC ACC GTG TGT GGC TGC AAG PAG AkC CA
1155	Wrong Nucleic Acid Designator	GCC GIC CTG TTG CCT CTG GTT ATC TTC CTA GGT
1155	# of Sequences for line conflicts w/ running total	GCC GIC CTG TTG CCT CTG GTT ATC TTC CTA GGT
1224	# of Sequences for line conflicts w/ running total	GGGAAGTGTG CCATCTGCTC CCAGACAGCT GAGGG
1235	Entered (461) and Calc. Seq. Length (0) differ	(A) LENGTH:461 amino acids
1236	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
1238	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:
1238	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:
1415	Entered (340) and Calc. Seq. Length (0) differ	(A) LENGTH:340 amino acids
1416	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
1418	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:
1418	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71: